

10/581773

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SEQUENCE LISTING

<110> Imperial College Innovations Limited
<120> Therapeutically Useful Molecules
<130> 28646/42100
<140> PCT/GB2004/005100
<141> 2004-12-06
<150> GB 0328363.7
<151> 2003-12-06
<160> 18
<170> SeqWin99
<210> 1
<211> 9
<212> PRT
<213> Artificial Sequence
<220>
<223> Peptide of WT1 which is presented by HLA-A2 class I molecules
<400> 1
Arg Met Phe Pro Asn Ala Pro Tyr Leu
1 5
<210> 2
<211> 6
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<213> Artificial Sequence
<220>
<223> CDR1 of human TCR V -1.5 (V -8.2)
<400> 2
Ser Ser Tyr Ser Pro Ser
1 5
<210> 3
<211> 7
<212> PRT
<213> Artificial Sequence
<220>
<223> CDR2 of human TCR V -1.5 (V -8.2)
<400> 3
Tyr Thr Ser Ala Ala Thr Leu
1 5
<210> 4
<211> 14
<212> PRT
<213> Artificial Sequence
<220>
<223> CDR3 of human TCR V -1.5 (V -8.2) - 1

<400> 4
Val Val Ser Pro Phe Ser Gly Gly Gly Ala Asp Gly Leu Thr
1 5 10

<210> 5
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 of human TCR V -1.5 (V -8.2) - 2

<400> 5
Ser Pro Phe Ser Gly Gly Gly Ala Asp Gly Leu Thr
1 5 10

<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 of human TCR V -2.1 (V -20.1)

<400> 6
Asp Phe Gln Ala Thr Thr
1 5

<210> 7
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 of human TCR V -2.1 (V -20.1)

<400> 7
Ser Asn Glu Gly Ser Lys Ala
1 5

<210> 8
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 of human TCR V -2.1 (V -20.1) - 1

<400> 8
Ser Ala Arg Asp Gly Gly Glu Gly
1 5

<210> 9
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 of human TCR V -2.1 (V -20.1) - 2

<400> 9
Arg Asp Gly Gly Glu Gly Ser Glu Thr Gln Tyr
1 5 10

<210> 10
 <211> 11
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Framework amino acid sequence of constant portion C-terminal to CDR3

 <400> 10
 Phe Gly Lys Gly Thr His Leu Ile Ile Gln Pro
 1 5 10

 <210> 11
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Beginning of constant region of human TCR V -1.5 (V -8.2)

 <400> 11
 Tyr Ile Gln Asn Pro
 1 5

 <210> 12
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Beginning of framework amino acid sequence of human TCR V -2.1 (V -20.1)

 <400> 12
 Ser Glu Thr Gln Tyr
 1 5

 <210> 13
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Part of framework amino acid sequence of human TCR V -2.1 (V -20.1)

 <400> 13
 Phe Gly Pro Gly Thr Arg Leu Leu Val Leu
 1 5 10

 <210> 14
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Part of constant region of human TCR V -2.1 (V -20.1)

 <400> 14
 Glu Asp Leu Lys Asn
 1 5

 <210> 15

<211> 830
 <212> DNA
 <213> Human TCR V -1.5 (V -8.2)

<400> 15
 atgctcctgc tgctcgtccc agtgctcgag gtgattttta ctctgggagg aaccagagcc 60
 cagtcggtga cccagcttga cagccacgtc tctgtctctg aaggaacccc ggtgctgctg 120
 aggtgcaact actcatcttc ttattcacca tctctcttct ggtatgtgca acaccccaac 180
 aaaggactcc agcttctcct gaagtacaca tcagcggcca ccttgggttaa aggcataaac 240
 ggttttgagg ctgaatttaa gaagagtga acctccttcc acctgacgaa accctcagcc 300
 catatgagcg acgcggctga gtacttctgt gttgtgagtc ctttttcagg aggaggtgct 360
 gacggactca cctttggcaa agggactcat ctaatcatcc agccctatat ccagaaccct 420
 gaccctgccc tgtaccagct gagagactct aaatccagt acaagtctgt ctgcctattc 480
 accgattttg attctcaaac aaatgtgtca caaagtaagg attctgatgt gtatatcaca 540
 gacaaaactg tgctagacat gaggtctatg gacttcaaga gcaacagtgc tgtggcctgg 600
 agcaacaaat ctgactttgc atgtgcaaac gccttcaaca acagcattat tccagaagac 660
 accttcttcc ccagcccaga aagtctctgt gatgtcaagc tggtcgagaa aagctttgaa 720
 acagatacga acctaaactt tcaaaacctg tcagtgattg gggtccgaat cctcctcctg 780
 aaagtggccc ggtttaatct gctcatgacg ctgcggctgt ggtccagctg 830

<210> 16
 <211> 276
 <212> PRT
 <213> Human TCR V -1.5 (V -8.2)

<400> 16
 Met Leu Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly
 1 5 10 15
 Gly Thr Arg Ala Gln Ser Val Thr Gln Leu Asp Ser His Val Ser Val
 20 25 30
 Ser Glu Gly Thr Pro Val Leu Leu Arg Cys Asn Tyr Ser Ser Ser Tyr
 35 40 45
 Ser Pro Ser Leu Phe Trp Tyr Val Gln His Pro Asn Lys Gly Leu Gln
 50 55 60
 Leu Leu Leu Lys Tyr Thr Ser Ala Ala Thr Leu Val Lys Gly Ile Asn
 65 70 75 80
 Gly Phe Glu Ala Glu Phe Lys Lys Ser Glu Thr Ser Phe His Leu Thr
 85 90 95
 Lys Pro Ser Ala His Met Ser Asp Ala Ala Glu Tyr Phe Cys Val Val
 100 105 110
 Ser Pro Phe Ser Gly Gly Gly Ala Asp Gly Leu Thr Phe Gly Lys Gly
 115 120 125
 Thr His Leu Ile Ile Gln Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val
 130 135 140
 Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe
 145 150 155 160
 Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp
 165 170 175
 Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe
 180 185 190
 Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys

195 200 205

Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro
210 215 220

Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu
225 230 235 240

Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg
245 250 255

Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg
260 265 270

Leu Trp Ser Ser
275

<210> 17
<211> 933
<212> DNA
<213> Human TCR V -2.1 (V -20.1)

<400> 17

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catccgagct	gggttatctg	taagagtggg	acctctgtga	agatcgagtg	ccgttccttg	120
gactttcagg	ccacaactat	gttttggtat	cgtcagttcc	cgaaacagag	tctcatgctg	180
atggcaactt	ccaatgaggg	ctccaaggcc	acatacgagc	aaggcgctcg	gaaggacaag	240
tttctcatca	accatgcaag	cctgaccttg	tccactctga	cagtgaccag	tgcccatcct	300
gaagacagca	gcttctacat	ctgcagtgtg	agagatgggg	gggaggggtc	ggagacccag	360
tacttcgggc	caggcacgcg	gctcctgggt	ctcgaggacc	tgaaaaacgt	gttcccaccc	420
gaggtcgctg	tgtttgagcc	atcagaagca	gagatctccc	acacccaaaa	ggccacactg	480
gtgtgcctgg	ccacaggctt	ctaccccgc	cacgtggagc	tgagctgggtg	ggtgaatggg	540
aaggaggtgc	acagtggggt	cagcacagac	ccgcagcccc	tcaaggagca	gcccgccttc	600
aatgactcca	gatactgcct	gagcagccgc	ctgaggggtc	cggccacctt	ctggcagaac	660
ccccgcaacc	acttccgctg	tcaagtccag	ttctacgggc	tctcggagaa	tgacgagtgg	720
accagggata	gggccaacc	tgtcacccag	atcgtcagcg	ccgaggcctg	gggtagagca	780
gactgtggct	tcacctccga	gtcttaccag	caaggggtcc	tgtctgccac	catcctctat	840
gagatcttgc	taggggaagg	caccttgat	gccgtgctgg	tcagtgccct	cgtgctgatg	900
gccatggtca	agagaaagga	ttccagaggc	tag			933

<210> 18
<211> 310
<212> PRT
<213> Human TCR V -2.1 (V -20.1)

<400> 18

Met Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala
1 5 10 15

Val Val Ser Gln His Pro Ser Trp Val Ile Cys Lys Ser Gly Thr Ser
20 25 30

Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe
35 40 45

Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser
50 55 60

Asn Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys
65 70 75 80

Phe Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr
85 90 95

Ser Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Arg Asp
 100 105 110
 Gly Gly Glu Gly Ser Glu Thr Gln Tyr Phe Gly Pro Gly Thr Arg Leu
 115 120 125
 Leu Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val
 130 135 140
 Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu
 145 150 155 160
 Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp
 165 170 175
 Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln
 180 185 190
 Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser
 195 200 205
 Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His
 210 215 220
 Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp
 225 230 235 240
 Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala
 245 250 255
 Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly
 260 265 270
 Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
 275 280 285
 Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys
 290 295 300
 Arg Lys Asp Ser Arg Gly
 305 310